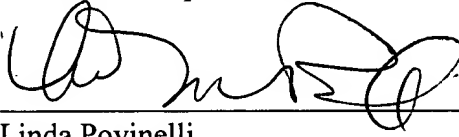




PATENT

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July 10, 2001
Date


Linda Povinelli

#22

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : B. Brett Finlay *et al.*
Application No. : 09/189,415
Filed : November 10, 1998
For : HOST RECEPTOR FOR PATHOGENIC BACTERIA

Examiner : S. Devi
Art Unit : 1645
Docket No. : 482112.402
Date : July 10, 2001

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Commissioner for Patents
Washington, DC 20231

RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT
APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID
SEQUENCE DISCLOSURES

Commissioner for Patents:

In response to the Notice to Comply With Requirements For Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures mailed June 27, 2001, Applicants submit the following:

- (1) Declaration regarding Sequence Listing;
- (2) Paper copy of Sequence Listing (11 pages);
- (3) Computer Readable Form of Sequence Listing; and

(4) Copy of Notice to Comply.

The enclosed Sequence Listing includes no new material and complies with the requirements for patent applications containing nucleotide sequence and/or amino acid sequence disclosures. Applicants respectfully submit that this application is now in compliance with 37 C.F.R. §§ 1.821-1.825 and WIPO Standard 25.



00500

PATENT TRADEMARK OFFICE

Respectfully submitted,

Seed Intellectual Property Law Group PLLC

Jeffrey C. Pepe, Ph.D.

Registration No. 46,985

Phone: (206) 622-4900

Fax: (206) 682-6031

JCP:Imp

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PTO/SB/21 (08-00)

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TRANSMITTAL FORM


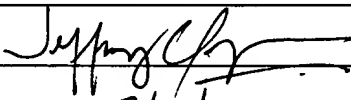
(To be used for all correspondence after initial filing)

Application Number	09/189,415
Filing Date	November 10, 1998
First Named Inventor	B. Brett Finlay
Group Art Unit	1645
Examiner Name	S. Devi
Attorney Docket No.	482112.402

ENCLOSURES (check all that apply)

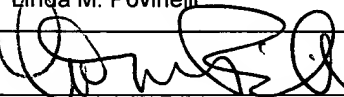
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Remarks		

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Individual Name	Jeffrey C. Pepe, Ph.D.	 00500 PATENT TRADEMARK OFFICE
Signature		
Date	7/10/01	

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231 on the date specified below.

Typed or printed name	Linda M. Povinelli	
Signature		Date: 7/10/01

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**FEE TRANSMITTAL
for FY 2001**

Patent fees are subject to annual revision.

TOTAL AMOUNT OF PAYMENT (\$)**620.00****Complete if Known**

Application Number	09/189,415
Filing Date	November 10, 1998
First Named Inventor	B. Brett Finlay
Examiner Name	S. Devi
Group Art Unit	1645
Attorney Docket No.	482112.402

METHOD OF PAYMENT

- 1.
- ☐
- The Commissioner is hereby authorized to charge indicated fees and credit any overpayments to:

Deposit Account Number
19-1090Deposit Account Name
Seed Intellectual Property Law Group PLLC

- ☒
- Charge Any Additional Fee Required Under 37 CFR 1.16 and 1.17 and credit any overpayment to Deposit Account Number above.

- ☒
- Applicant claims small entity status. See 37 CFR 1.27

- 2.
- ☒
- Payment Enclosed:

☒ Check ☐ Credit card ☐ Money Order ☐ Other**FEE CALCULATION****1. BASIC FILING FEE**

Large Entity		Small Entity		Fee Description	Fee Paid
Fee Code	Fee (\$)	Fee Code	Fee (\$)		
101	710	201	355	Utility filing fee	
106	320	206	160	Design filing fee	
107	490	207	245	Plant filing fee	
108	710	208	355	Reissue filing fee	
114	150	214	75	Provisional filing fee	
SUBTOTAL (1)					(\$)

2. EXTRA CLAIM FEES

		Extra Claims	Fee from below	Fee Paid
Total Claims		** =	X	=
Independent Claims		** =	X	=
Multiple Dependent			X	=

Large Entity		Small Entity		Fee Description
Fee Code	Fee (\$)	Fee Code	Fee (\$)	
103	18	203	9	Claims in excess of 20
102	80	202	40	Independent claims in excess of 3
104	270	204	135	Multiple dependent claim, if not paid
109	80	209	40	** Reissue independent claims over original patent
110	18	210	9	** Reissue claims in excess of 20 and over original patent

SUBTOTAL (2) (\$)

**or number previously paid, if greater; For Reissues, see above

FEE CALCULATION (continued)**3. ADDITIONAL FEES**

Large Entity		Small		Fee Description	Fee Paid
Fee Code	Fee (\$)	Fee Code	Fee (\$)		
105	130	205	65	Surcharge - late filing fee or oath	
127	50	227	25	Surcharge - late provisional filing fee or cover sheet.	
139	130	139	130	Non-English specification	
147	2,520	147	2,520	For filing a request for <i>ex parte</i> reexamination	
112	920*	112	920*	Requesting publication of SIR prior to Examiner action	
113	1,840*	113	1,840*	Requesting publication of SIR after Examiner action	
115	110	215	55	Extension for reply within first month	
116	390	216	195	Extension for reply within second month	
117	890	217	445	Extension for reply within third month	
118	1,390	218	695	Extension for reply within fourth month	
128	1,890	228	945	Extension for reply within fifth month	
119	310	219	155	Notice of Appeal	
120	310	220	155	Filing a brief in support of an appeal	
121	270	221	135	Request for oral hearing	
138	1,510	138	1,510	Petition to institute a public use proceeding	
140	110	240	55	Petition to revive - unavoidable	
141	1,240	241	620	Petition to revive - unintentional	620
142	1,240	242	620	Utility issue fee (or reissue)	
143	440	243	220	Design issue fee	
144	600	244	300	Plant issue fee	
122	130	122	130	Petitions to the Commissioner	
123	130	123	130	Petitions related to provisional applications	
126	180	126	180	Submission of Information Disclosure Stmt	
581	40	581	40	Recording each patent assignment per property (times number of properties)	
146	710	246	355	Filing a submission after final rejection (37 CFR § 1.129(a))	
149	710	249	355	For each additional invention to be examined (37 CFR § 1.129(b))	
179	710	279	355	Request for Continued Examination (RCE)	
169	900	169	900	Request for expedited examination of a design application	

Other fee (specify) _____

*Reduced by Basic Filing Fee Paid

SUBTOTAL (3) (\$)**620****SUBMITTED BY**Name (Print/Type) **Jeffrey C. Pepe**Registration No. **46,985**
Attorney/Agent)Firm Name/
Address

Signature

Date

7/10/01**00500**

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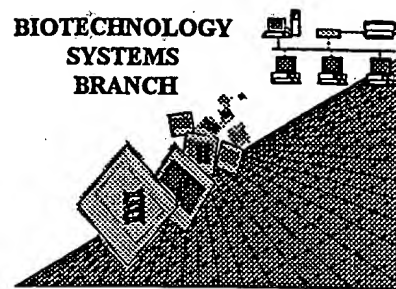
V. Ryan

O I P E JC176
JUL 13 2001
OFFICE

RAW SEQUENCE LISTING

ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/189,415

Art Unit / Team No. :

1641

Date Processed by STIC:

3/10/2000

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THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

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JUL 13 2001

Application No.: 09/189,415

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

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Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/189,415

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

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V. Ryan

1641

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/189,415

DATE: 03/10/2000
TIME: 15:42:36

Input Set: I189415.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

P. 2

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2 Kenny, Brendan
3 DeVinney, Rebekah
4 Stein, Markus
5 <120> TITLE OF INVENTION: HOST RECEPTOR FOR PATHOGENIC BACTERIA
6 <130> FILE REFERENCE: 07422/013001
7 <140> CURRENT APPLICATION NUMBER: US/09/189,415
8 <141> CURRENT FILING DATE: 1998-11-10
9 <150> EARLIER APPLICATION NUMBER: 60/065,130
10 <151> EARLIER FILING DATE: 1997-11-12
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PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/189,415

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TIME: 15:42:36

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58      20          25          30
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60      35          40          45
61      Leu Phe Ser Pro Leu Arg Asn Ser Met Ala Asp Ser Val Asp Ser Arg
62      50          55          60
63      Asp Ile Pro Gly Leu Pro Thr Asn Pro Ser Arg Leu Ala Ala Ala Thr
64      65          70          75          80
65      Ser Glu Thr Cys Leu Leu Gly Gly Phe Glu Val Leu His Asp Lys Gly
66      85          90          95
67      Pro Leu Asp Ile Leu Asn Thr Gln Ile Gly Pro Ser Ala Phe Arg Val
68      100         105         110
69      Glu Val Gln Ala Asp Gly Thr His Ala Ala Ile Gly Glu Lys Asn Gly
70      115         120         125
71      Leu Glu Val Ser Val Thr Leu Ser Pro Gln Glu Trp Ser Ser Leu Gln
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73      Ser Ile Asp Thr Glu Gly Lys Asn Arg Phe Val Phe Thr Gly Gly Arg
74      145         150         155         160
75      Gly Gly Ser Gly His Pro Met Val Thr Val Ala Ser Asp Ile Ala Glu
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77      Ala Arg Thr Arg Ile Leu Ala Lys Leu Asp Pro Asp Asn His Gly Gly
78      180         185         190
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83      Asn Ser Ser Val Arg Ser Asp Pro Lys Phe Trp Val Ser Val Gly Ala
84      225         230         235         240
85      Ile Ala Ala Gly Leu Ala Gly Leu Ala Ala Thr Gly Ile Ala Gln Ala
86      245         250         255
87      Leu Ala Leu Thr Pro Glu Pro Asp Asp Pro Thr Thr Thr Asp Pro Asp
88      260         265         270
89      Gln Ala Ala Asn Ala Ala Glu Ser Ala Thr Lys Asp Gln Leu Thr Gln
90      275         280         285
91      Glu Ala Phe Lys Asn Pro Glu Asn Gln Lys Val Asn Ile Asp Ala Asn
92      290         295         300
93      Gly Asn Ala Ile Pro Ser Gly Glu Leu Xaa Asp Asp Ile Val Glu Gln
94      305         310         315         320

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W-->

all item 10
on Enn summary
sheet

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/189,415

DATE: 03/10/2000
TIME: 15:42:36

Input Set: I189415.RAW

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104   385                      390                      395                      400
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106              405                      410                      415
107   Val Ala Leu Met Pro Gln Glu Arg Arg Arg Phe Ser Asp Arg Arg Asp
108              420                      425                      430
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112              450                      455                      460
113   Ala His Gln Pro Glu Glu His Ile Tyr Asp Glu Val Ala Ala Asp Pro
114   465                      470                      475                      480
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116              485                      490                      495
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<212> TYPE: DNA

<213> ORGANISM: Escherichia coli

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132   ccgttgggat ctctgctgct atttacgctt gtaaggaatt ctatggctga ttctggcgac 180
133   aatcgtgccg gtgatgttcc tggacttcct gtaaaccgca tgcgcctggc ggcgtctgag 240
134   ataactctga atgatggatt tgaagttctt catgatcatg gtccgctcga tactcttaac 300
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137   ttgcagtcca ttgatcctga aggtaaagac aaatttgtat ttactggagg ccgtggtggt 480
138   gctgggcatg ctatggtcac cgttgcttca gatatacagg aagcccgcca aaggatactg 540
139   gagctgttag agcccaaagg gaccggggag tccaaagggt ctggggagtc aaaaggcggt 600
140   ggggagttga gggagtcaaa tagcgggtgcg gaaaacacca cagaaactca gacctcaacc 660
141   tcaacttcca gccttcgttc agatcctaaa ctttggttgg cggtggggac tgttgctaca 720
142   ggtctgatag gggtggcggc gacgggtatt gtacaggcgc ttgcattgac gccggagccg 780
143   gatagcccaa ccacgaccga ccctgatgca gctgcaagtg caactgaaac tgcgacaaga 840
144   gatcagttaa cgaaagaagc gttccagaac ccagataatc aaaaagttaa tatcgatgag 900

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147   caaaaaaaaa atgatgaaca acaagctaaa cgccaggagg agctgaaagt ttcacgggg 1080
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153   gttaaaacat cgctgcatga ttgcgagggt cgcacttcta attctaatac gtctgttcag 1440
154   aatatgggga atacagattc tgttgatat agcaccattc aacatcctcc cggggatact 1500
155   actgataacg gcgcacggtt attaggaaat ccaagtgcgg ggattcaaag cacttatgcy 1560
156   cgtctggcgc taagtgggtg attacgccat gacatgggag gattaacggg ggggagtaat 1620
157   agcgtgtgta atacttcgaa taaccacca gcgcgggat cccatcggtt cgtctaaata 1680
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<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 4

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167           20           25           30
168   Gly Gln Leu Ile Asn Ser Thr Gly Pro Leu Gly Ser Arg Ala Leu Phe
169           35           40           45
170   Thr Pro Val Arg Asn Ser Met Ala Asp Ser Gly Asp Asn Arg Ala Ser
171           50           55           60
172   Asp Val Pro Gly Leu Pro Val Asn Pro Met Arg Leu Ala Ala Ser Glu
173           65           70           75           80
174   Ile Thr Leu Asn Asp Gly Phe Glu Val Leu His Asp His Gly Pro Leu
175           85           90           95
176   Asp Thr Leu Asn Arg Gln Ile Gly Ser Ser Val Phe Arg Val Glu Thr
177           100          105          110
178   Gln Glu Asp Gly Lys His Ile Ala Val Gly Gln Arg Asn Gly Val Glu
179           115          120          125
180   Thr Ser Val Val Leu Ser Asp Gln Glu Tyr Ala Arg Leu Gln Ser Ile
181           130          135          140
182   Asp Pro Glu Gly Lys Asp Lys Phe Val Phe Thr Gly Gly Arg Gly Gly
183           145          150          155          160
184   Ala Gly His Ala Met Val Thr Val Ala Ser Asp Ile Thr Glu Ala Arg
185           165          170          175
186   Gln Arg Ile Leu Glu Leu Leu Glu Pro Lys Gly Thr Gly Glu Ser Lys
187           180          185          190
188   Gly Ala Gly Glu Ser Lys Gly Val Gly Glu Leu Arg Glu Ser Asn Ser
189           195          200          205
190   Gly Ala Glu Asn Thr Thr Glu Thr Gln Thr Ser Thr Ser Thr Ser Ser
191           210          215          220
192   Leu Arg Ser Asp Pro Lys Leu Trp Leu Ala Leu Gly Thr Val Ala Thr
193           225          230          235          240
194   Gly Leu Ile Gly Leu Ala Ala Thr Gly Ile Val Gln Ala Leu Ala Leu

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198	Ser	Ala	Thr	Glu	Thr	Ala	Thr	Arg	Asp	Gln	Leu	Thr	Lys	Glu
199				275				280				285		
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201				290				295				300		
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203												315		320
204	Gln	Ala	Lys	Ala	Ala	Gly	Glu	Glu	Ala	Lys	Gln	Gln	Ala	Ile
205												330		335
206	Asn	Ala	Gln	Ala	Gln	Lys	Lys	Tyr	Asp	Glu	Gln	Gln	Ala	Lys
207														350
208	Glu	Glu	Leu	Lys	Val	Ser	Ser	Gly	Ala	Gly	Tyr	Gly	Leu	Ser
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210	Leu	Ile	Leu	Gly	Gly	Gly	Ile	Gly	Val	Ala	Val	Thr	Ala	Ala
211														380
212	Arg	Lys	Asn	Gln	Pro	Val	Glu	Gln	Thr	Thr	Thr	Thr	Thr	Thr
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214	Thr	Thr	Thr	Ser	Ala	Arg	Thr	Val	Glu	Asn	Lys	Pro	Ala	Asn
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216	Pro	Ala	Gln	Gly	Asn	Val	Asp	Thr	Pro	Gly	Ser	Glu	Asp	Thr
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224	Arg	Ile	Trp	Gly	Ile	Gln	Ile	Ser	Val	Val	Tyr	Ser	Thr	Ile
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226	Pro	Pro	Arg	Asp	Thr	Thr	Asp	Asn	Gly	Ala	Arg	Leu	Leu	Gly
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228	Ser	Ala	Gly	Ile	Gln	Ser	Thr	Tyr	Ala	Arg	Leu	Ala	Leu	Ser
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230	Leu	Arg	His	Asp	Met	Gly	Gly	Leu	Thr	Gly	Gly	Ser	Asn	Ser
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241	aaaggggggc	ttgatactct	taactctgct	attggatctt	cgttattccg	tggtgaaact	180							
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Line ? Error/Warning

Original Text

93 W "N" or "Xaa" used: Feature required

Gly Asn Ala Ile Pro Ser Gly Glu Leu Xaa A